NCBI

PubMed www.pubmed.gov

A service of the National Library of Medicine and the National Institutes of Health

My NCBI [Sign In] [Register]

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Books

Search PubMed for Go Clear

Limits Preview/Index History Clipboard Details

Display Citation Show 20 Sort by Send to

All: 1 Review: 0

About Entrez
NCBI Toolbar

Text Version

Entrez PubMed
Overview
Help | FAQ
Tutorials
New/Noteworthy
E-Utilities

PubMed Services
Journals Database
MeSH Database
Single Citation Matcher
Batch Citation Matcher
Clinical Queries
Special Queries
LinkOut
My NCBI

Related Resources
Order Documents
NLM Mobile
NLM Catalog
NLM Gateway
TOXNET
Consumer Health
Clinical Alerts
ClinicalTrials.gov
PubMed Central

1: Cell. 2001 Sep 21;106(6):745-57.

Related Articles, Links

Cell Press

Structural basis for autoinhibition of the Ephb2 receptor tyrosine kinase by the unphosphorylated juxtamembrane region.

Wybenga-Groot LE, Baskin B, Ong SH, Tong J, Pawson T, Sicheri F.

Program in Molecular Biology and Cancer, Samuel Lunenfeld Research Institute, Mount Sinai Hospital, 600 University Avenue, Ontario M5G 1X5, Toronto, Canada.

The Eph receptor tyrosine kinase family is regulated by autophosphorylation within the juxtamembrane region and the kinase activation segment. We have solved the X-ray crystal structure to 1.9 A resolution of an autoinhibited, unphosphorylated form of EphB2 comprised of the juxtamembrane region and the kinase domain. The structure, supported by mutagenesis data, reveals that the juxtamembrane segment adopts a helical conformation that distorts the small lobe of the kinase domain, and blocks the activation segment from attaining an activated conformation. Phosphorylation of conserved juxtamembrane tyrosines would relieve this autoinhibition by disturbing the association of the juxtamembrane segment with the kinase domain, while liberating phosphotyrosine sites for binding SH2 domains of target proteins. We propose that the autoinhibitory mechanism employed by EphB2 is a more general device through which receptor tyrosine kinases are controlled.

MeSH Terms:

- Amino Acid Sequence
- Amino Acid Substitution
- Animals
- Binding Sites
- Cell Membrane/physiology*
- Comparative Study
- Crystallography, X-Ray
- Humans
- Mice
- Models, Molecular
- Molecular Sequence Data
- Mutagenesis, Site-Directed
- Phosphorylation
- Protein Conformation
- Protein Structure, Secondary
- Receptor Protein-Tyrosine Kinases/antagonists & inhibitors
- Receptor Protein-Tyrosine Kinases/chemistry*
- Receptor Protein-Tyrosine Kinases/metabolism*
- Receptor, EphB2
- Recombinant Proteins/antagonists & inhibitors
- Recombinant Proteins/chemistry
- Recombinant Proteins/metabolism
- Research Support, Non-U.S. Gov't
- Sequence Alignment
- Sequence Homology, Amino Acid

Substances:

- Recombinant Proteins
- Receptor Protein-Tyrosine Kinases
- Receptor, EphB2

Secondary Source ID:

- PDB/1JPA

PMID: 11572780 [PubMed - indexed for MEDLINE]

Display Citation Show 20 Sort by Send to

Write to the Help Desk
NCBI | NLM | NIH
Department of Health & Human Services
Privacy Statement | Freedom of Information Act | Disclaimer

Mar 13 2006 06:33:20

potential art

NCBI PubMed www.pubmed.gov

A service of the National Library of Medicine and the National Institutes of Health

My NCBI [Sign In] [Regis

All Databases PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Bool

Search PubMed for Go Clear

Limits Preview/Index History Clipboard Details

Limits: **Publication Date from 1999 to 2000**

Display Abstract Show 20 Sort by Send to

All: 1 Review: 0

About Entrez
NCBI Toolbar

Text Version

Entrez PubMed
Overview
Help | FAQ
Tutorials
New/Noteworthy
E-Utilities

PubMed Services
Journals Database
MeSH Database
Single Citation Matcher
Batch Citation Matcher
Clinical Queries
Special Queries
LinkOut
My NCBI

Related Resources
Order Documents
NLM Mobile
NLM Catalog
NLM Gateway
TOXNET
Consumer Health
Clinical Alerts
ClinicalTrials.gov
PubMed Central

1: Mol Cell Biol. 1990 Dec;10(12):6316-24.

Related Articles, Links

FREE full text article in PubMed Central

cDNA cloning and characterization of eck, an epithelial cell receptor protein-tyrosine kinase in the eph/elk family of protein kinases.

Lindberg RA, Hunter T.

Molecular Biology and Virology Laboratory, Salk Institute for Biological Studies, San Diego, California 92186-5800.

A human epithelial (HeLa) cDNA library was screened with degenerate oligonucleotides designed to hybridize to highly conserved regions of protein-tyrosine kinases. One cDNA from this screen was shown to contain a putative protein-tyrosine kinase catalytic domain and subsequently used to isolate another cDNA from a human keratinocyte library that encompasses the entire coding region of a 976-amino-acid polypeptide. The predicted protein has an external domain of 534 amino acids with a presumptive N-terminal signal peptide, a transmembrane domain, and a cytoplasmic domain of 418 amino acids that includes a canonical protein-tyrosine kinase catalytic domain. Molecular phylogeny indicates that this protein kinase is closely related to eph and elk and that this receptor family is more closely related to the non-receptor protein-tyrosine kinase families than to other receptor protein-tyrosine kinases. Antibodies raised against a TrpE fusion protein immunoprecipitated a 130-kDa protein that became phosphorylated on tyrosine in immune complex kinase assays, indicating that this protein is a bona fide protein-tyrosine kinase. Analysis of RNA from 13 adult rat organs showed that the eck gene is expressed most highly in tissues that contain a high proportion of epithelial cells, e.g., skin, intestine, lung, and ovary. Several cell lines of epithelial origin were found to express the eck protein kinase at the protein and RNA levels. Immunohistochemical analysis of several rat organs also showed staining in epithelial cells. These observations prompted us to name this protein kinase eck, for epithelial cell kinase.

PMID: 2174105 [PubMed - indexed for MEDLINE]

Display Abstract Show 20 Sort by Send to

100% alignment w/ SEQ ID NO: 1

10/601,324

Write to the Help Desk
NCBI | NLM | NIH
Department of Health & Human Services
Privacy Statement | Freedom of Information Act | Disclaimer

Mar 13 2006 04:32:14